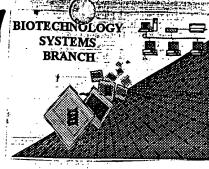
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Application Serial Number:

09/265,5400

Source:

1643

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

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The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

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Raw Sequence Listing Error-Summary

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE The number/text at the end of each line "wrapped" down to the next line. Wrapped Nucleics RECEIVED This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The amino acid number/text at the end of each line "wrapped " down to the next line. Wrapped Aminos This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". TIECH CEXTER Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces. The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Misaligned Amino Acid between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Numbering Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Variable Length contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" . Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. Skipped Sequences Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). Skipped Sequences missing. If intentional, please use the following format for each skipped sequence. Sequence(s) (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. (NEW RULES) In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Use of <213>Organism are missing this mandatory field or its response. (NEW RULES) Use of <220>Feature Sequence(s) ____ are missing the <220>Feature and associated headings. (NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

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file, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence tisting).

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/03/2001 TIME: 12:53:41

TECH CENTER 1600/2900

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Output Set: N:\CRF3\01022001\1265540C.raw

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         Moore, Kevin W.
          Murgolo, Nicholas J.
         Bazan, J. Permando
 8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 10 <130> FILE REFERENCE: DX0804K
 12 KL405 CURRENT APPLICATION NUMBER: 09/265.540C
 13 <141> CUFFENT FILING DATE: 1999-03-08
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61 agalgaetga galggaeaga algethlatt tiggaaagaa acaalghich agateaauct 120
63 gagteracea a ato eag act tto aca ato gtt eta gaa gaa ato too aca. 170
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001 TIME: 12:53:41

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Output Set: N:\CRF3\01022001\1265540C.raw

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	69		1.5					20					25									1 1	
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`	roo	GLY.	atg Mèt	gag : Gl.u	atc Ile	ńcc Xaa	aaa Lys	nat Xaa	ggc Gly	ttc	cac	ctg Leu	gtt Val	att Ile	gag Glu	cta	gag Glu	602	le one	al	lien	am	40
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(a) (c)	101 103 104 105	gac gac Asp	et.g	: Glu : qgg : Gly 160	atc Ile 145 ccc Pro	ńce Xaa Cag Gln	ttt Phe	Xaa gag Glu	tte Phe	ttc Phe 150 ett Leu	Gac His gtg Val	Teu gcc Ala	Val tac Tyr	tqq Trp	155 asg Xaa	ctg Leu agg Arg	gan Glu	602 650	lesse	al de	ligh viet	an ly e	ero erder
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() }	101 103 104 105 107 108 109 111 112	gac Asp cen Pro gtg Val	etg Leu qqt Gly 175 cac	Glu Gly Gly 160 gcc Ala	atc Ile 145 ccc Pro gag Glu	ncc Xaa Cag Gln qaa	ttb Phe cat His	: Xaa : gag : Glu : qtc : Val : 180 : gag	tte the Phe 165 and Lys	ttc Phe 150 ctt Leu atg	cac His gtg Val gtq Val	Geu Geo Ala agg Arg gea Ala	tac Tyr aqt. Ser 185	tgg Trp 170 ggg Gly	Glu 155 asg Xaa ggt Gly	Leu agg Arg att	gan Glu cca Pro		lesse avids con	de de	ligh irect	andly e	nder uder vdon.
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QC.	101 103 104 105 107 108 109 111 112 113 115 116	gac Asp cet Pro gtg Val 190 caq Gln	etg Leu qqt Gly 175 cac His	Glu Ggg Gly 160 gcc Ala cta Leu ttc	atc Ile 145 ccc Pro gag Glu gaa Gtu gtg Val	fice Xaa Gag Gln qaa Glu acc Thr aag Lys 210	ttb Phe cat His atg Met 195 gcc Ala	gag Glu qtc Val 180 gag Glu att	tte Phe 165 awa Lys cca Pro 939 Gly	ttc Phe 150 ott Leu atq Met ggg Gly arg Xaa	cac His gtg Val gtq Val gct Ala tac Tyr 215	Geo Ala agg Arg gea Ala 200 age Ser	tac Tyr aqt Ser 185 tac Tyr gcc Ala	tqq Trp 170 999 Gly tqt Cys	Glu 155 asg Xaa ggt Gly gtg Val agc Ser	etg Leu agg Arg ant The agg Lys cag Gin 220	gag Glu cda Pro qcc Ala 205 aca Thr	746	lesse aeds con	de de	reet orde	andly e	nder uder vdon.
	101 103 104 105 107 108 109 111 112 113 115 116 117	gac Asp cert Pro gtg Val 190 cag Gln	ctg Leu qqt Gly 175 cac nis aca Thr	eta ttc phe	atc Ile 145 ccc Pro gag Glu gaz Gtu gtg Val	fice Xaa Gag Gln qaa Glu acc Thr aag Lys 210 gtg	tttt Phe cat His arg Mot 195 gdc Ala	: Xaa : gag : Glu : qtc : Val 180 gag : Glu att Ile	tte Phe 165 aaa Lys cca Pro 999 Gly	ttc Phe 150 ctt Leu atq Met ggg Gly arg Xaa	gtg Val gtq Val gcf Ala tac Tyr 215	Geu geo Ala agg Arg gea Ala 200 age Ser	tac Tyr aqt Ser 185 tac Tyr gcc Ala	tgg Trp 170 ggg Gly tgt Cys	Glu 155 asg Xaa ggt Gly gtg Val agc Ser	etg Leu agg Arg att Tie agg Lys cag Gin 220	gag Glu coa Pro gcc Ala 205 aca Thr	746	lesse avdr con	de de	veet orde	andly e	nder uder uden.
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OK,	100 1 100 1	gae Asp cert Pro gtg Val 190 cag Gln gaa Glu	etg Leu qqt Giy 175 cac His aca Thr tqt Cys	e Glu e ggg 160 gcc Ala cta teu ttc Phe qtg Val	atc Ile 145 cocc Pro gag Glu gaa Glu gtg Val gar Xaa 225 gtt	fice Xaa Gag Gln qaa Giu acc Thr aag Lys 210 gtg Val	ttb Phe cat His arg Met 195 gec Ala caa Gln	gag Glu Qtc Val 180 gag Glu att Ile qaa Gly	tte Phe 165 aaa Lys cca Pro 999 Gly gaq Glu ctg	Phe 150 ott Leu atg Met ggg GLy arg Xaa goo Ala 230 aho	cac His gtg Val gtq Val gct Ala tac Tyr 215 att Tle	que Ala agg Arg gea Ala 200 age Ser cec Pro	tac Tyr aqt Ser 185 tac Tyr gcc Ala otq Leu	tigg Trp 170 999 Gly tight Cys ttc Phe gta Val	Glu 155 asg Xaa ggt Gly gtg Val agc Ser ctg Leu 235 cca	Leu agg Arg att The agg Lys cag Gin 220 gcc Ala	gag Glu eca Pro gcc Ala 205 aca Thr ctg Leu	746 794 842	lesse aeids con	de de	ligh ired	and ly e	nder under
OK,	100 1 100 1	gac Asp cer Pro gtg Val 190 Gln gaa Glu	etg Leu ggt Giy 175 cac His aca Thr tqt Cys	equation of the control of the contr	atc Ile 145 ccc Pro quq Glu gaz Glu gtg Val qar Xaa 225 gtt Val	cag Glu acc Thr aag Lys 210 gtg Val	Lys tttt Phe cat His arg Mot 195 goc Ala caa Gln ttc Phe	: Xaa : gag : Glu qtc Val 180 gag Glu alt Ile qqa Gly alt	tte Phe 165 aaa Lys cca Pro ggg Gly gag Glu ctg Leu 245	Phe 150 ctt Leu atg Met 999 GLy arg Xaa 900 Ala 230 alte 1ie	dac His gtg Val gtg Val gtg Val tac Tyr 215 att Tle ctr Leu	geo Ala agg Arg gea Aia 200 agg Ser cec pro gtg yal	tac Tyr aqt Ser 185 tac Tyc goo Ala otq teu gtc val	tggg Trp 170 ggg Gly tgt Cys ttc Phe gta Val gtg Val 250	Glu 1555 asg Xaa gfg Gly gfg Val agc Ser otg Leu 235 coa Pro	ctg Leu agg Arg atr Tle agg Lys cag Gin 220 gcc Ala ctg Leu	gag Glu oga Pro gcc Ala 205 aca Thr ctg Leu	746 794 842 890	lesse aeds con	de de	veet vode	and ly e	nder inder
OK,	100 L 101 L	gac Asp cert Program of the State St	etgg GLy 175 cac Ris aca Thr tqt Cys	ggg Gly 169 gcc Ala cta Leu ttc Phe qtg Val	atc Ile 145 ccc Pro quq Glu gaa Glu gtg Val qar Xaa 225 gtt Val atg	cag Gln qaa Glu acc Thr Lys 210 gtg Val	tttt Phe cat His atgg Mot 195 good Ala caa Gln ttc Phe	: Xaa : gag : Glu qtcc Val 180 gag Glu att tle qqa Gly att tct cttq	tte Phe 165 aaa Eys cea Pro 994 Gly gaq Glu ctg 245 otto	Phe 150 ctt Leu atg Met 999 Kaa 900 Ala 230 atc tie	dac His gtg Val gtg Val gtg Val tac Tyr 215 att. Tle ctr Leu tac	gea agg Arg gea Ala 200 agg Ser cec glg glg Val	tac Tyr aqt Ser 185 tac Tyc goo Ala otq gtc Val	tqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	Glu 155 asg Xaa ggtg Gly gtg Val agc Ser ctg Leu 235 cca Pro	ctg Leu agg Arg ann The agg Lys cag Gin 220 gcc Ala ctg Leu	gag Glu coa Pro qec Ala 205 aca Thr ctg Leu	746 794 842	lesse aeds con	de de	veet orde	and ly e	nder inder indon.
OK.	100 L 101 L	gac Asp cert Program of the State St	etgg GLy 175 cac Ris aca Thr tqt Cys	ggg Gly 169 gcc Ala cta Leu ttc Phe qtg Val	atc Ile 145 ccc Pro quq Glu gaa Glu gtg Val qar Xaa 225 gtt Val atg	cag Glu acc Thr aag Lys 210 gtg Val	tttt Phe cat His atgg Mot 195 good Ala caa Gln ttc Phe	: Xaa : gag : Glu qtcc Val 180 gag Glu att tle qqa Gly att tct cttq	tte Phe 165 aaa Eys cea Pro 994 Gly gaq Glu ctg 245 otto	Phe 150 ctt Leu atg Met 999 Kaa 900 Ala 230 atc tie	dac His gtg Val gtg Val gtg Val tac Tyr 215 att. Tle ctr Leu tac	gea agg Arg gea Ala 200 agg Ser cec glg glg Val	tac Tyr aqt Ser 185 tac Tyc goo Ala otq gtc Val	tqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	Glu 155 asg Xaa ggtg Gly gtg Val agc Ser ctg Leu 235 cca Pro	ctg Leu agg Arg ann The agg Lys cag Gin 220 gcc Ala ctg Leu	gag Glu coa Pro qec Ala 205 aca Thr ctg Leu	746 794 842 890	lesse avis con	de de	veet orde	and ly e	nder inder

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/265,540C

DATE: 01/02/2001

TIME: 12:53:41

inpul Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

131 glo clo cha gae ace tig ada ata are wat low coe day dag tig ate 132 Val Leu Pro Asp Thr Leu Lys He Thr Ash Ser Pro Gla Lys Leu He 133 270 275 280 135 age the aga age gag gag gtg gut gee tgt gee ang get gtg atg tet 1034 136 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser 137 390 295 300 139 cet gag gaa cle etc aga que lgu ale tea taugitique quagquecea 1084 140 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser 141. 305 3.10 143 ggfyaageeg agaacetggt etgealyaea tygaaaeeat gaggggacaa gtbybyttte 1144 145 tgttiteege cacqqaeaag qgatgagaqa agtagqaaga gcctgttgte tacaagteta 1204 147 quaqcaacca teaquqqeaq qqtqqtitqt ckaucaquac.aaptquetqa qqytakrqqq 1264 149 gwtgtgaeet etagaetkyg ggstkseayt igewtgaytg ageaaccetg ggaaaagtga 2324 12-51 cttcatccct tnggtccnaa gttttctcat ctgtaatggg ggatncctac aaaactg 154 <240> SEQ TD NO: 2 155 <211> LENGTH: 311 156 <212> TYPE: PRT 157 <213> ORGANISM: primate 159 <400> SEQUENCE: 2 160 Met Gin Thr Phe Thr Met Val Leu Glu Glu Ele Trp Thr Ser Leu Phe 163 Met. Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val 164 20 25 30166 Ala 11e beu Pro Ala Pro Gin Ash beu Ser Val ben Ser Thr Ash Met 35 4.0 169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val 5.0 172 Tyr Tyr Ser Val Glu Tyr Glu Gly Glu Tyr Glu Ser Leu Tyr Thr Ser 70 75 175 His The Trp The Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu 85 90 178 Cys Asp Val Thr Asp Asp Tie Thr Ala Thr Val Pro Tyr Ash Leu Arg 1.00 105 181 Val Arg Ala Thr Lou Gly Sor Glo Thr Ser Ala Trp Ser Ile Leu Lys 1.15 120 125 184 His Pro Phe Asn Arg Asn Ser Thr Hie Len Thr Arg Pro Gly Met Glu 135 1.40 W--> 187 Ile (Xaa) Lys (Xaa) Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly 150 W--> 190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp(Xaa)Arg Glu Pro Gly Ala 165 -17a 🖳 193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly 41e Pro Val His Leu 194 180 185190 196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gin Thr Phe 197 195 200 205 199 Val Lys Ala Ile Gly(Xaa) Tyr Ser Ala Phe Ser Cln Thr Glu Cys Val 200 斉 210 215 350 W--> 202(Xa) Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe

SU den 10 on Eva Summay Sheet RAW SEQUENCE LISTING PATENT APPLICATION: US/09/265,540C

DATE: 01/03/2001 TIME: 12:53:41

Input Set : A:\804k.app

Output Set: N:\CRF3\01022001\1265540C.raw

205 Val GL/ Phe Met Len Ite Leu Val Val Val Pro Leu Phe Val Trp Lys 206 245 250 208 Met GI; Arg Leu Leu Glm Tyr Ser Cys Cys Pro Val Val Val Leu Pro 209 260 265 270 211 Asp Thr Low Lys The Thr Asm Ser Pro Gli Lys Lew He Ser Cys Arg 212 2.15 280 285 214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu 215 290 295 300 217 Leu Leu Arg Ala Trp Ile Ser 218 303 221 <210> SEQ ID NO: 3 222 <211> LENGTH: 1244 223 <210> TYPE: DNA 224 <213> ORCANTSM: primate 226 <220> PEATURE: 227 <221> NAME/REY: COS 228 <222> LOCATION: (2)..(694) 230 <400> SEQUENCE: 3 231 close equation gas coalege globege of gather one tog off acalgde out 49 232 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro 1.0 1.5 235 tyg the cup tee lot tyg aar ytt acc ant gag cet eet gag age ale 236 Trp Phe Leu Ser Cys Trp Asn Val Thr Lie Gly Pro Pro Glu Ser Lie 237 20 25 30 239 tgq gtg acg ccq gga gaa gor too oto ato ato agg tto too tot ccc 240 Trp Val Thr Pro Gly Glu Ala Ser Leu Lie The Arg Phe Ser Ser Pro 241 35 4.0 4.5 243 the gas are see see and sta gas tat the sag has hat give can bay 244 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa 245 50 55 6.0 247 tgq qaa asq gog qga ato caa asq ytt asa ggt cot tto asq ago aac 248 Trp Clu Lys Ala 317 Ile Gin Lys Val Lys Gly Pro Phe Lys Ser Asn 249 65 70 75 251 nee are gry try gat ggo try aga eee htm aga gaa tae tyt htm cua 252 Ser The Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln 85 9.0 255 gtg aag geg cat ote fift ego aca foo tigo aac acc for agg eee gge 256 Val Lys Ala His Len Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly 257 105 1.1,0 259 ego tia ago aac ata act tgo tao gaa aca atg atg gat goo act acg 260 Arg Geo Ser Asn 11e Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr 261 115 120 125 263 aad eft caa caa qte atc etc atc goo gtg gga gtc tit otg teg etg 264 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu 265 130 135 140 267 ged ded out ded dad goe tot the the end gut out aga the bas dec 268 Ala Ala Lou Ala Cly Cly Cys Phe Phe Lou Val Lou Arg Tyr Lys Cly 269 145 150 155 166 271 etg gtg dan tac tyg tit cac tot deg den age ate dea tem can ate 524

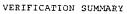


RAW SEQUENCE LISTING DARE: 01/02/2001
PATENT APPLICATION: US/09/265,540C TIME: 12:53:44

Imput Set : A:\804k.app

Output Sot: N:\CRF3\01022001\1265540C.raw

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     276 Glu Glu Pyr Leu Lys Asp Pro Ser Glu Pro 11e Leu Glu Ala Leu Asp
                    180
                                    185
                                                           1.90
     279 dag dae deg ted een dea gat gat gee tig dae tig gig fet git git
     280 bys Asp Thr Ser Pro Thr Asp Asp Ala Tip Asp Len Val Ser Val Val
     281 195
                          200
     283 year tit oca gen ang gay caa gan gat git con can ago act tig acc
     284 Ala Phe Pro Ala bys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
                               215
                                                 220
     287 can and tot got god gto tgo tagoctytag ggtuaggget etgagecgag
                                                                         724
     288 Glm Asm Ser Gly Ala Val Cys
     289 225
                          230
     291 gaagetgetg algleealot cageactita tygaateegg teelecalit Ferlyteece 784
     293 adaaggcccy teagtgeetg tgaagatgta acgygtetea tyggggegae aagestattg 844
     205 attititet teaaactaug agtititetaa teataegegi tititagaara attetaeaga 904
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     200 goaaatggge qtotggcaeq octotgaran titttegtra grayeragga racgaggter 1024
     301 cotontigal gaugecoote gggcagaeca tgtcacetgi eccageeige cocaagaagg 1081
     303 gacattaagt qqoocticti catateeaaa caeetygott gaaatgiqai ragooctota 1144
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         20
                                      25
     322 Trp Val Thr Pro Gly Glu Ata Ser Leu Ile ILe Arg Phe Ser Ser 323 35 40 15
W--> 325 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
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     328 Trp Glu Lys Ala Gly He Gla Lys Val Lys Gly Pro Phe Lys Ser Asn
     329 65
                          70
                                               7.5
     331 Set fle Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gfu 332 $90$
     334 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
     335
                1 (10)
                                105
     337 Arg Leu Ser Asn 41e Thr C7s Tyr Glu Thr Met Met Asp Ala Fbr Thr 338 $1.15 . $120 $125
     340 Lys Led Gln Gln Val Tie Lou Tie Ala Val Giy Val Phe Leu Ser Leu
     311 130
                              135
     343 Ala Ala Leu Ala Gly Gly Cys the Phe Leu Val Leu Arg Tyr Lys Gly
                           150
                                            155
     346 Leu Val bys Tyr Trp Phe His Ser Pro Pro Ser He Pro Ser Glm 11e
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PAPENT APPLICATION: US/09/265,540C

DATE: 01/02/2001 P1ME: 12:53:42

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Output Set: N:\CRF3\01022001\1265540C.raw

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m M})258~{
m W};$ Mandatory Peature missing, <221> not found for SEQ 10%(2)1.:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ 1Df:2 $15:187~\mathrm{M}:258~\mathrm{W}:$ Mandatory Feature missing, <223> not found for SEQ 1D#:2 L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ 1D \pm :2 L:190 M:258 W: Mandator Feature missing, <220> not found for SEQ 1D \pm :2 1.:190 N:258 W: Mandatory Feature missing, <221> not found for SEQ 1Ds:2 To: 190 M: 258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2 12:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ FD#:2 M:340 Repeated in SeqNo=2 La:199 M:258 W: Mandatory Feature missing, <220> not found for SEO ID#:2 Ea:199 M:258 W: Mandatory Feature missing, <221> not found for SEO ID#:2 La:199 M:258 W: Mandatory Feature missing, <222> not found for SEO ID#:2 $\rm Li:199~M:258~W:$ Mandatory Feature missing, <223> not found for SEQ ID#:2 ${\rm Li}(202~{\rm M})258~{\rm W};$ Mandatory Feature missing, <220> not found for SMO LD#:2 L:202 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2 T.:202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2 LE:202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2 La:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3 Ta: 244 M: 340 W: (46) "n" or "Xaa" used: Feature regulated, for SEO ID#:3 1.:325 H:258 W: Mandatory Feature missing, <220> not found for SEO ID#:4 f.:325 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4 $C_{\rm F}(325~{\rm M};258~{\rm W};$ Mandatory Feature missing, <222> not found for SEQ TDE:4 L.: 325 M: 258 W: Mandatory Feature missing. <323> not found for SEQ ID#:4 $\rm L_{2}(325~\rm M;340~\rm W;~(46)~\rm ''n''$ or "Xaa" used: Feature required, for SEO ID#:4